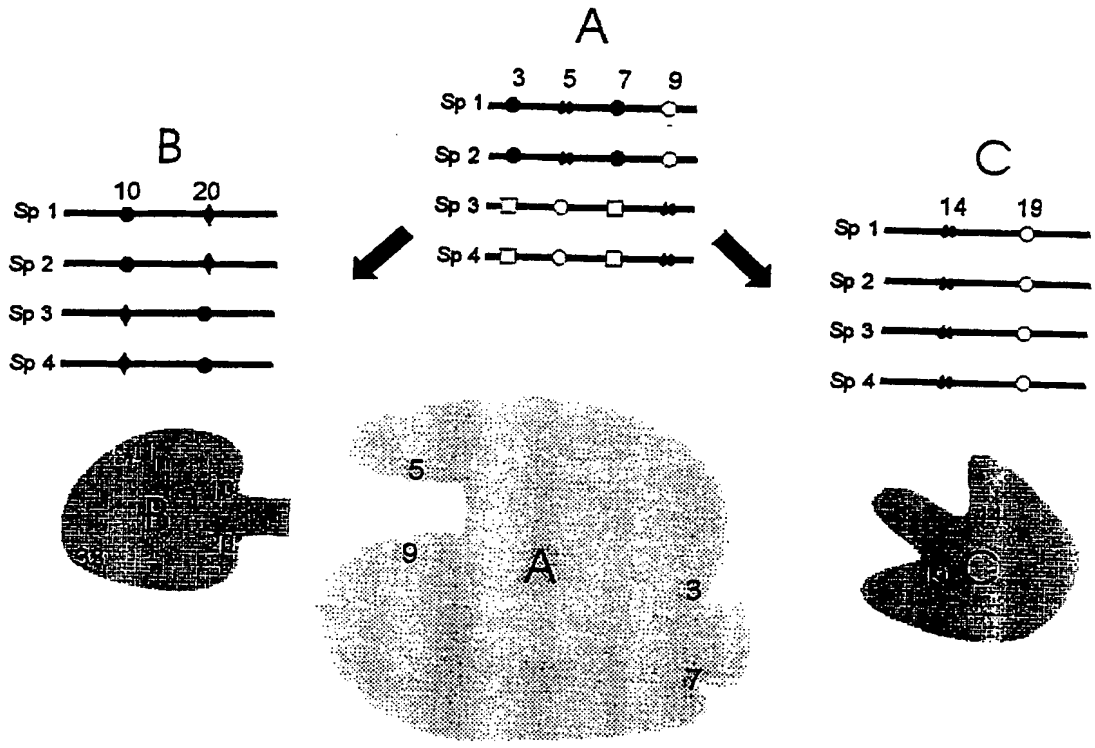
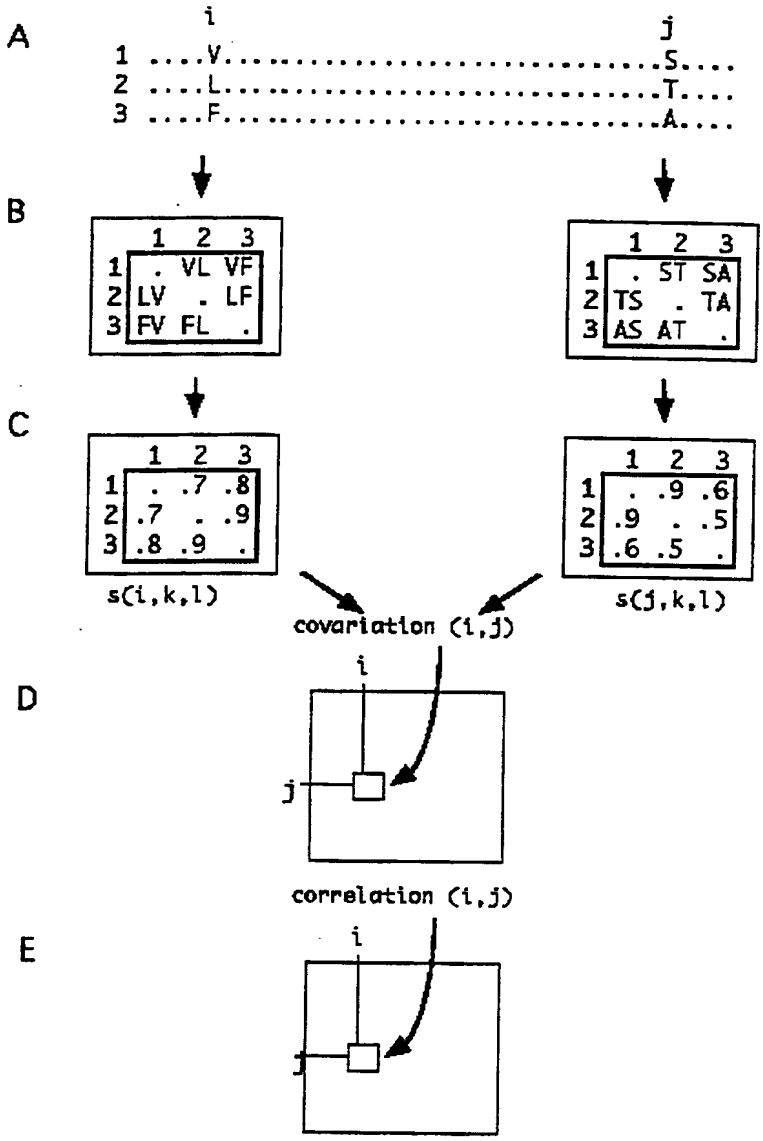
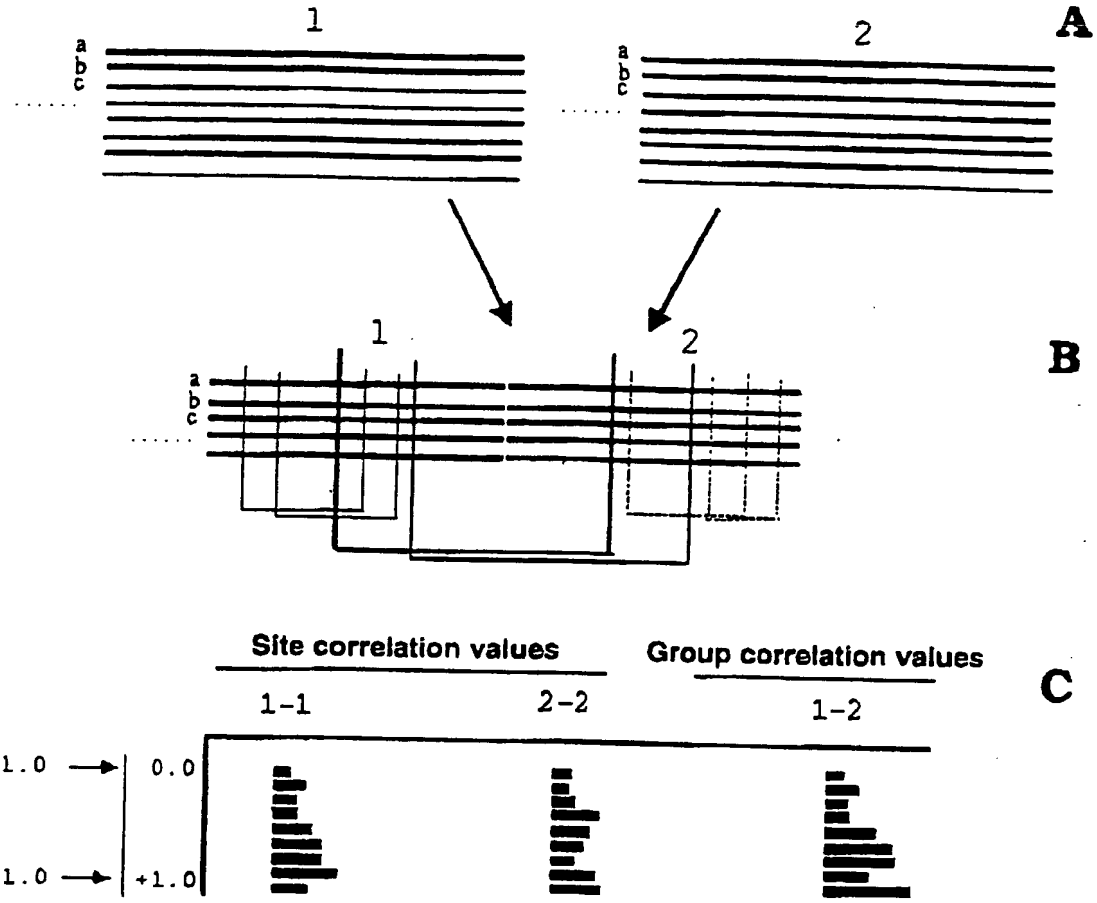

A
3 5 7 9
Sp 1
Sp 2
Sp 3
Sp 4
B
10 20
Sp 1
Sp 2
Sp 3
Sp 4
C
14 19
Sp 1
Sp 2
Sp 3
Sp 4
5
9
A
3
7

FIG. 1


A
i
j
1 ....V.....S....
2 ....L.....T....
3 ....F.....A....
B
1 2 3
1 . VL VF
2 LV . LF
3 FV FL .
1 2 3
1 . ST SA
2 TS . TA
3 AS AT .
C
1 2 3
1 . .7 .8
2 .7 . .9
3 .8 .9 .
s(i,k,l)
1 2 3
1 . .9 .6
2 .9 . .5
3 .6 .5 .
s(j,k,l)
covariation (i,j)
D
i
j
correlation (i,j)
E
i
j

F I G. 2



D

$$C_{12} = \sum_{i=0.0}^{1.0} \frac{P_{12i}}{P_{11i} + P_{22i}} \; i$$

E

$$S_{12} = \frac{C_{12} - \overline{C}_1}{\sigma_1}$$

FIG. 3

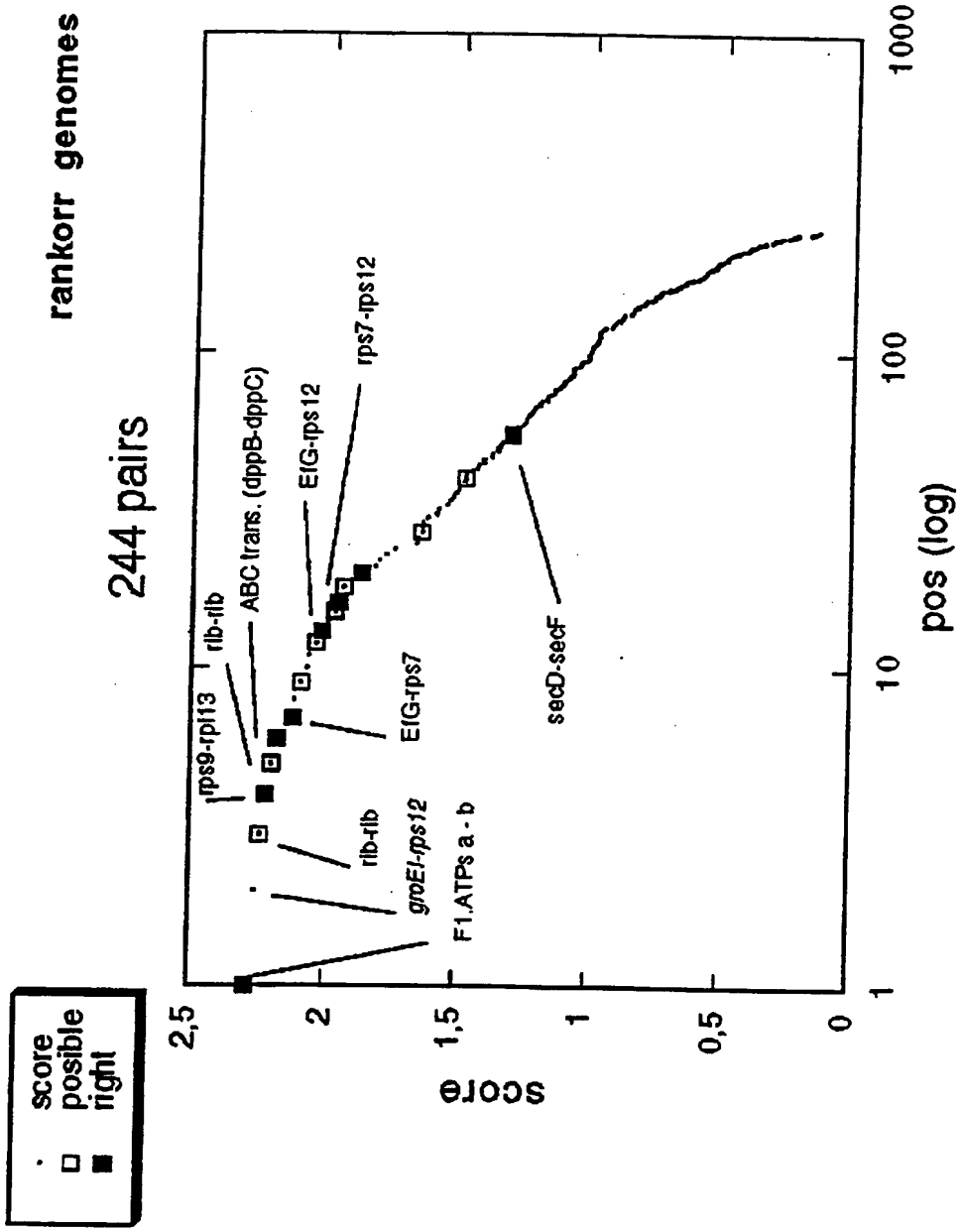
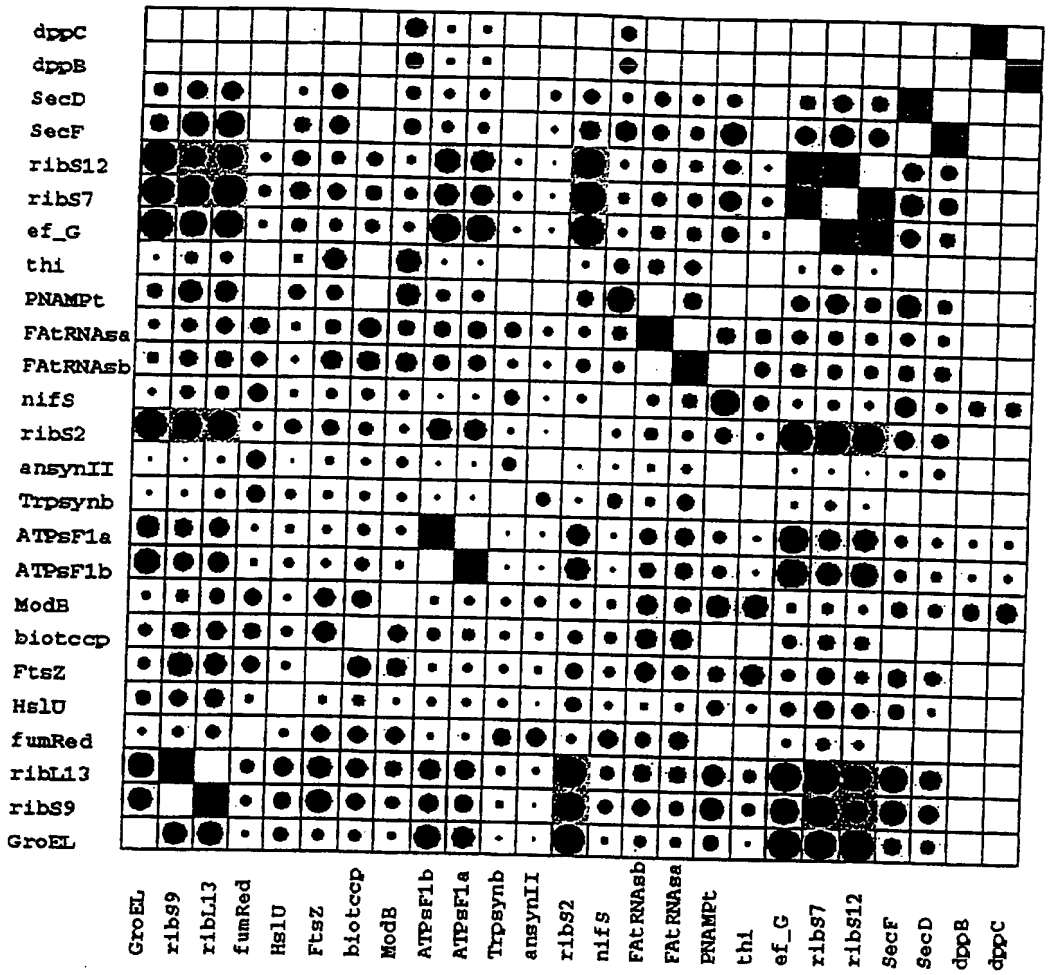

rankorr genomes
244 pairs
score
posible
right
rps9-rpl13
rib-rib
ABC trans. (dppB-dppC)
EfG-rps12
rps7-rps12
rib-rib
groEl-rps12
F1,ATPs a - b
EfG-rps7
secD-secF
2,5
2
1,5
1
0,5
0
score
1000
100
10
1
pos (log)

FIG. 4


dppC
dppB
SecD
SecF
ribS12
ribS7
ef_G
thi
PNAMPt
FAtRNAsa
FAtRNAsb
nifS
ribS2
ansynII
Trpsynb
ATPsF1a
ATPsF1b
ModB
biotccp
FtsZ
HslU
fumRed
ribL13
ribS9
GroEL
GroEL
ribS9
ribL13
fumRed
HslU
FtsZ
biotccp
ModB
ATPsF1b
ATPsF1a
Trpsynb
ansynII
ribS2
nifS
FAtRNAsb
FAtRNAsa
PNAMPt
thi
ef_G
ribS7
ribS12
SecF
SecD
dppB
dppC

F I G. 5